

GenCore version 5.1.1.8
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OM protein - protein search, using sw model

Run on: May 20, 2006, 20:19:26 ; Search time 298 Seconds
(without alignments)
450.091 Million Cell updates/sec

Title: US-10-705-716A-2
Perfect score: 767
Sequence: 1 MCGGSRADAIETPRYESTWT.....VTENIRQMDRSKRVTKNCIN 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 92501592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_7.2.*

1: uniprot_spot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	767	100.0	145	Q920K5_RAT	Q920K5 rattus norv
2	746	97.3	145	Q8VHV1_MOUSE	Q8VHV1 mus musculus
3	645	84.1	145	Q9HA93_HUMAN	Q9HA93 homo sapien
4	634	82.7	145	Q8WNE9_PIG	Q8WNE9 sus scrofa
5	617.5	80.5	180	Q8WXS3_HUMAN	Q8WXS3 homo sapien
6	473.5	61.7	149	Q8WXS1_HUMAN	Q8WXS1 homo sapien
7	459	59.8	123	Q9CYS9_MOUSE	Q9CYS9 mus musculus
8	294	38.3	54	Q790N3_RAT	Q790N3 rattus norv
9	294	38.3	54	Q8VBS8_MOUSE	Q8VBS8 mus musculus
10	288	37.5	73	Q8WXS0_HUMAN	Q8WXS0 homo sapien
11	278	36.2	54	Q8WTP6_HUMAN	Q8WTP6 homo sapien
12	272	35.5	80	Q8WXS2_HUMAN	Q8WXS2 homo sapien
13	267	34.8	54	Q8WNE8_PIG	Q8WNE8 sus scrofa
14	166.5	21.7	51	Q4RR60_TETNG	Q4RR60 tetraodon n
15	161	21.0	32	Q801V5_BRARE	Q801V5 brachydanio
16	160.5	20.9	36	Q4ST12_TETNG	Q4ST12 tetraodon n
17	92.5	12.1	613	Q6ZMJ6_HUMAN	Q6ZMJ6 homo sapien
18	92.5	12.1	753	CNOT3_HUMAN	Q75175 homo sapien
19	92.5	12.1	1073	PVDA_PLAKN	P22545 plasmodium
20	89.5	11.7	177	Q4Q487_LEIMA	Q4Q487 leishmania
21	89	11.6	281	Q3W1F9_9ACTO	Q3W1F9 frankia sp.
22	88	11.5	365	POLG_SUMUS	P25242 sugarcane m
23	87	11.3	1035	Q76C74_YEAST	Q76C74 saccharomyc
24	87	11.3	1713	Q8TGE1_YEAST	Q8TGE1 saccharomyc
25	86.5	11.3	397	Q4DTZ6_TRYCR	Q4DTZ6 trypanosoma
26	86.5	11.3	554	Q4HWN0_GIBBEZ	Q4HWN0 gibberella
27	86.5	11.3	1195	Q5BBD7_EMENI	Q5BBD7 aspergillus
28	86	11.2	585	Q7UZ29_RHOBA	Q7UZ29 rhodospirell
29	86	11.2	1070	FVUG29_PLAKN	F50494 plasmodium
30	86	11.2	1894	Q4Q515_LEIMA	Q4Q515 leishmania
31	85.5	11.1	733	Q4QGH8_LEIMA	Q4QGH8 leishmania

32	85	11.1	450	2	Q2QLT5_ORYZA	Q2QLT5 oryza sativ
33	85	11.1	507	2	Q4LTE7_9BURK	Q4LTE7 burkholderi
34	85	11.1	932	2	Q3F8F8_9BURK	Q3F8F8 burkholderi
35	84.5	11.0	534	2	Q96SA2_HUMAN	Q96SA2 homo sapien
36	84	11.0	155	2	Q6USF5_PLAFA	Q6USF5 plasmodium
37	84	11.0	408	2	Q4D6E3_TRYCR	Q4D6E3 trypanosoma
38	83.5	10.9	214	2	Q8WTC3_LEUMA	Q8WTC3 leucophaea
39	83.5	10.9	341	2	Q31MK3_SYN7	Q31MK3 synecococc
40	83.5	10.9	341	2	Q5MZC6_SYN6	Q5MZC6 synecococc
41	83.5	10.9	677	2	Q6A015_MOUSE	Q6A015 mus musculu
42	83.5	10.9	700	2	Q30678_XANMA	Q30678 xanthomonas
43	83.5	10.9	751	1	CNOT3_MOUSE	Q8K0V4 mus musculu
44	83.5	10.9	953	1	Q5BATS_EMENI	Q5BATS aspergillus
45	83	10.8	314	2	Q5BEH2_EMENI	Q5BEH2 aspergillus

ALIGNMENTS

RESULT 1
Q920K5_RAT PRELIMINARY; PRT; 145 AA.
AC Q920K5_...
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 15.
DE Dem-A20-4 (BAALC isoform 1-6-8).
GN Name=dem-A20-4; Synonyms=BaalC;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridea; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=1559234; DOI=10.1111/j.1471-4159.2004.02902.x;
RA Wang X., Tian Q.B., Okano A., Sakagami H., Moon I.S., Kondo H.,
RA Endo S., Suzuki T.;
RT "BAALC 1-6-8 protein is targeted to postsynaptic lipid rafts by its N-terminal myristoylation and palmitoylation, and interacts with a, but not b, subunit of Ca2+/calmodulin-dependent protein kinase II.";
RL J. Neurochem. 92:647-659(2005).
[2]
NUCLEOTIDE SEQUENCE.
STRAIN=Sprague-Dawley;
RC MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinen K.,
RA Mrozek K., Sill H., Khuttila S., Koltz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de La Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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EMBL; AB073318; BAB70507.1; -; mRNA.
EMBL; AF3171321; AAL50517.1; -; mRNA.
DR Ensembl; ENSRNOG00000004697; Rattus norvegicus.
DR RGD; 628703; Baalc.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
SQ SEQUENCE 145 AA; 15475 MW; D5A27AD67456F341 CRC64;

Query Match 100.0%; Score 767; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 9.2e-61;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MCGGSRADAIETPRYESTWTETSTWLTYSDALPSAAATDSGPAGGLHAGVLEDGP	60
Db	1	MCGGSRADAIETPRYESTWTETSTWLTYSDALPSAAATDSGPAGGLHAGVLEDGP	60
QY	61	SSNGVLRPAAPFGIANPEKKNCGTCPCNSQSLSSGPLTQKQNGLWTTTEAKRDAKMSAR	120

DB 61 SSGVLRPAAGGIANPEKKNQCTQCPNSQSLSSGTLTKQKGLWTEAKRDAKMSAR 120
 QY 121 EVAISVTENIRQMDRSKRVTNKCIN 145
 DB 121 EVAISVTENIRQMDRSKRVTNKCIN 145
 RECLT 2
 Q8VHV1_MOUSE
 ID Q8VHV1_MOUSE PRELIMINARY; PRT; 145 AA.
 AC Q8VHV1;
 DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
 DT 07-FEB-2005, entry version 19.
 DE BAALC isoform 1-6-8 (16 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:19630028H16 product:brain and acute leukemia, cytoplasmic, full insert sequence).
 DE Name=Baalcl;
 GN Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; OC Muridae; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=12956/SVETAC;
 RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
 RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K., Mrozek K., Sill H., Knuutila S., Koltz J.E., Archer K.J., Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
 RT "BAALC, the human member of a novel mammalian neuroectoderm gene lineage, is implicated in hematopoiesis and acute leukemia.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning.";
 RL Methods Enzymol. 303:19-44(1999).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX PubMed=16141072; DOI=10.1126/science.1112014;
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N., Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K., Bajic V.B., Brenner S.E., Batalov S., Forrest A.R., Zavolan M., Davis M.J., Wilming L.G., Aidinis V., Allen J.E., Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L., Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M., Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R., de Bernardi D., Della E., Dalrymple B.P., de Bono B., Della Gatta G., Fletcher C.F., Fukushima T., Furuno M., Fagiolini M., Faulkner G., Georgi-Hemming P., Gingeras T.R., Gojobori T., Green R.E., Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N., Hill D., Humineck L., Iacono M., Ikeo K., Iwama A., Ishikawa T., Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H., Kitano H., Kollas G., Krishnan S.P., Kruger A., Kummerfeld S.K., Kurochkin I.V., Laureau L.F., Lazarevic D., Lipovich L., Liu J., Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L., Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K., Mottagui-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P., Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O., Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G., Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M., Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C., Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y., Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B., Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K., Tannoja K., Tan S.W., Tang S., Taylor M.S., Tegner J., Teichmann S.A., Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,

Yamanashi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C., Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J., Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y., Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T., Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N., Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N., Nishio T., Okada M., Plessy C., Shibata K., Shiraki T., Suzuki S., Tegami M., Waki K., Watahiki A., Okamura-Oho Y., Suzuki H., Kawai J., Hayashizaki Y.;
 RT "The transcriptional landscape of the mammalian genome.";
 RL Science 309:1559-1563(2005).
 RN [4]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX PubMed=16141073; DOI=10.1126/science.1112009;
 RG RIKEN Genome Exploration Research Group, and Genome Science Group (Genome Network Core Team) and the FANTOM Consortium;
 RT "Antisense Transcription in the Mammalian Transcriptome.";
 RL Science 309:1564-1566(2005).
 RN [5]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kiyosawa H., Nikaide I., Osato N., Saito R., Suzuki H., Yamanaka I., Gojobori T., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Frazer K.S., Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M., Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wilming L.G., Wyshaw-Boris A., Yanagisawa M., Yang I., Yang L., Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y., Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K., Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S., Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A., Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 RN [6]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=C57BL/6J; TISSUE=Cerebellum;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J., Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,

Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
[7]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Kanno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
[8]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Kanno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer.";
Genome Res. 10:1757-1771(2000).
[9]
NUCLEOTIDE SEQUENCE.
STRAIN=C57BL/6J; TISSUE=Cerebellum;
Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
Hori F., Imotani K., Iijima Y., Itoh M., Kagawa I., Kasukawa T.,
Kato H., Kawai J., Kohji Y., Kondo S., Konno H., Kouda M., Koya S.,
Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
Tomaru A., Tota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (APR-2002) to the ENBL/GenBank/DBJ databases.

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ENBL; AF371320; AAL50516.1; -; mRNA.
ENBL; AK079337; BAC37611.1; -; mRNA.
MGI; MGI:1928704; Baalc.
GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR009728; BAALC.N.
DR Pfam; PF06989; BAALC.N; 1.
SQ SEQUENCE 145 AA; 15515 MW; 4972670A618C4D6D CRC64;

Query Match 97.3%; Score 746; DB 2; Length 145;
Best Local Similarity 97.2%; Pred. No. 7e-59;
Matches 141; Conservative 2; Mismatches 2; Indels 0; Gaps 0

QY 1 MGC0GSRADALEPRYSWTRTETSTWLTYYTDSALPSAAATDSGPEAGGLHAGVLEDCP 60
DQ |||||
QY 1 MGC0GSRADALEPRYSWTRTETSTWLTYYTDSALPSAAATDSGPEAGGLHAGVLEDCP 60
DQ |||||
QY 61 SSNGVLPAAPGGIANPEKKNCGTCPCNSQLSSGPLTKQNGLWTTTAKDKAKMSAR 120
DQ |||||
QY 61 SSNGVLPAAPGGIANPEKKNCGTCPCNSQLSSGPLTKQNGLWTTTAKDKAKMSAR 120
DQ |||||
QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
DQ |||||
DQ 121 EVAINVTEINIRQMDRSKRVTKNCIN 145

RESULT 3
Q9HA93 HUMAN PRELIMINARY; PRT; 145 AA.
ID Q9HA93 HUMAN

Q9HA93;
DT 01-MAR-2001, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2001, sequence version 1.
DT 07-MAR-2006, entry version 22.
DE Hypothetical protein FLJ12015 (BAALC isoform 1-6-8) (BAALC protein)
DE (BAALC 1-6-8).
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo
OX NCBI_TaxID=9606;
[1]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Whole embryo;
RC PubMed=14702039; DOI=10.1038/ng1285;
RX Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hoshiro T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata S., Watanabe M., Hiroaka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fuji A., Hara H., Tanase T.-O., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu P., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujitani T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs".
RL Nat. Genet. 36:40-45(2004).
[2]
RN NUCLEOTIDE SEQUENCE.
RP MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RX Tanner S.M., Austin J.L., Leone G., Rugh L.J., Plass C., Heironen K.,
RA Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de La Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RT Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
[3]
RN NUCLEOTIDE SEQUENCE.
RP TISSUE=Brain;
RX MEDLINE=21388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodríguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).
RN [4]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RG NIH MGC Project;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AK022077; BAB13960.1; -; mRNA.
DR EMBL; AF371319; AAL50515.1; -; mRNA.
DR EMBL; BC011517; AAL11517.1; -; mRNA.
DR EMBL; AF363578; AAL50377.1; -; Genomic DNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N.1.
DR CDS; CDS_1;
SQ SEQUENCE 145 AA; 15551 MW; CFB92BBE283DD92E CRC64;
Query Match 84.1%; Score 645; DB 2; Length 145;
Best Local Similarity 83.4%; Pred. No. 7.9e-50;
Matches 121; Conservative 10; Mismatches 14; Indels 0; Gaps 0;
QY 1 MCGGSRADAEIPRYESWTRETESTWLTYSALPSAAATDGPAGGLHAGVLEDGP 60
DB 1 MCGGSRADAEIPRYESWTRETESTWLTYSALPSAAATDGPAGGLHAGVLEDGP 60
QY 61 SSSGVLPAAPGGIANPEKKNCGTQCPNSQSLSSGGLPTQKQGLWTTEAKRDARMSAR 120
DB 61 PSNGVPRSTAPGGTNPKEKNCETQCPNPSLSSGGLPTQKQGLWTTEAKRDARMSAR 120
QY 121 EVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 EVTINVTDSIQMDRSRRITKNCYN 145
RESULT 4
Q8WNE9_PIG PRELIMINARY; PRT; 145 AA.
AC Q8WNE9
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE BAALC isoform 1-6-8.
GN Name=BAALC;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub.
OX NCBI_TaxID=9823;
SQ SEQUENCE 145 AA; 15551 MW; CFB92BBE283DD92E CRC64;
Query Match 80.5%; Score 617.5; DB 2; Length 180;
Best Local Similarity 67.2%; Pred. No. 3e-47;
Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;
QY 1 MCGGSRADAEIPRYESWTRETESTWLTYSALPSAAATDGPAGGLHAGVLEDGP 60
DB 1 MCGGSRADAEIPRYESWTRETESTWLTYSALPSAAATDGPAGGLHAGVLEDGP 60
QY 54 -----GVLEDPSSNGVLPAAPGGIANPEKKNCGT 85
DB 61 KIKAPDTSVSDGLFSAKMAPLAVFSGHMGLEDGLPSNGVPRSTAPGGIPNPKKNCET 120
QY 86 QCPNSQSLSSGGLPTQKQGLWTTEAKRDARMSARVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 QCPNPSLSSGGLPTQKQGLWTTEAKRDARMSARVAISVTENIRQMDRSKRVTKNCIN 145
RESULT 6
Q8WXS1_HUMAN PRELIMINARY; PRT; 149 AA.
AC Q8WXS1
ID Q8WXS1
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE BAALC 1-5-6-8.
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de La Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
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CC -----
DR EMBL; AF363578; AAL50379.1; -; Genomic DNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR HGNC; HGNC:14333; BAALC.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N.1.
SQ SEQUENCE 180 AA; 19224 MW; 380183E0F188F684 CRC64;
Query Match 80.5%; Score 617.5; DB 2; Length 180;
Best Local Similarity 67.2%; Pred. No. 3e-47;
Matches 121; Conservative 10; Mismatches 14; Indels 35; Gaps 1;
QY 1 MCGGSRADAEIPRYESWTRETESTWLTYSALPSAAATDGPAGGLHAGVLEDGP 60
DB 1 MCGGSRADAEIPRYESWTRETESTWLTYSALPSAAATDGPAGGLHAGVLEDGP 60
QY 54 -----GVLEDPSSNGVLPAAPGGIANPEKKNCGT 85
DB 61 KIKAPDTSVSDGLFSAKMAPLAVFSGHMGLEDGLPSNGVPRSTAPGGIPNPKKNCET 120
QY 86 QCPNSQSLSSGGLPTQKQGLWTTEAKRDARMSARVAISVTENIRQMDRSKRVTKNCIN 145
DB 121 QCPNPSLSSGGLPTQKQGLWTTEAKRDARMSARVAISVTENIRQMDRSKRVTKNCIN 145
RESULT 6
Q8WXS1_HUMAN PRELIMINARY; PRT; 149 AA.
AC Q8WXS1
ID Q8WXS1
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 07-FEB-2006, entry version 10.
DE BAALC 1-5-6-8.
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de La Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
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DR EMBL; AF363578; AAL50379.1; -; mRNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR HGNC; HGNC:14333; BAALC.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N.1.
SQ SEQUENCE 145 AA; 15401 MW; C75ED7D00BF02E26 CRC64;
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DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE BAALC 1-5-6-7-8.
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Archer K., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Koltz J.B., Placher K.J.,
RA Caligiuri M.A., Bloomfield C.D., de La Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia."
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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CC -----
DR EMBL; AF363578; AAL50381.1; -; Genomic DNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR InterPro; IPR009728; BAALC.N.
DR Pfam; PF06989; BAALC.N; 1.
SQ SEQUENCE 149 AA; 15577 MW; DB26C19969B91P6E CRC64;

Query Match 61.7%; Score 473.5; DB 2; Length 149;
Best Local Similarity 66.0%; Pred. No. 1.9e-34;
Matches 95; Conservative 2; Mismatches 12; Indels 35; Gaps 1;

QY 1 MCGGSRADAIPRYVSWTRETSTWLTYSDDALPSAAATDSCPEAGGLHA----- 53
DB 1 MCGGSRADAIPRYVSWTRETSTWLTYSDDALPSAAATDSCPEAGGLHVSLEAKS 60
QY 54 -----GVLEDGSPSSVGLRPAAPGGIANPEKKONCGT 85
DB 61 KIKAPTDSVSDGLFSASQWAPLAFVSHGMLDGLPSGVPRSTAPGGIPNPEKTKNCT 120
QY 86 QCPNSQSLSSGPLTKQNGLWTTTE 109
DB 121 QCPNPQSLSSGPLTKQNGLOTTE 144

RESULT 7
Q9CY99_MOUSE PRELIMINARY; PRT; 123 AA.
AC Q9CY99;
DT 01-JUN-2001, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2001, sequence version 1.
DT 07-FEB-2006, entry version 18.
DE 10, 11 days embryo whole body cDNA, RIKEN full-length enriched
DE library, clone:2810457D07 product:brain and acute leukemia,
DE cytoplasmic, full insert sequence.
GN Name=BaalC;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1016/S0076-6879(99)03004-9;
RX MEDLINE=99279253; PubMed=10349636;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning."
RL Methods Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1126/science.1112014;
RX PubMed=16141072;
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RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,
RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzius R., Shimokawa K.,
RA Bajic V.B., Bremner S.E., Batalov S., Forrest A.R., Zavolan M.,
RA Davis M.J., Wilming L.G., Aidinis V., Allen J.E.,
RA Ambesi-Impiombato A., Arweiler R., Aturaliya R.N., Bailey T.L.,
RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,
RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,
RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,
RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,
RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,
RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,
RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,
RA Hill D., Hummel L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,
RA Jakt M., Kanapin A., Katoh M., Kawasawa Y., Keiso J., Kitamura H.,
RA Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,
RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,
RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,
RA Matada H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,
RA Mottagui-Farar S., Mulder N., Nakano N., Nakachi H., Ng P.,
RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,
RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavese G., Pesole G.,
RA Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,
RA Rost B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,
RA Schonbach C., Sekiguchi K., Semple C.A., Seno S., Sessa L., Sheng Y.,
RA Shibusata Y., Shimada H., Shimada K., Silva D., Sinclair B.,
RA Sperling S., Stupka E., Sugura K., Sultana R., Takenaka Y., Taki K.,
RA Tannoja K., Tan S.K., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,
RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,
RA Yananishi H., Zabarovsky E., Zhu S., Zimmer A., Hide W., Bult C.,
RA Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,
RA Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,
RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,
RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,
RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Ninomiya N.,
RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,
RA Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J.,
RA Hayashizaki Y.;
RT "The transcriptional landscape of the mammalian genome."
RL Science 309:1559-1563(2005).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RX STRAIN=C57BL/6J; TISSUE=whole body; DOI=10.1038/nature01266;
RX MEDLINE=22354683; PubMed=12466851;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA Nitaide I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA Yagi K., Tomaru Y., Hasegawa Y., Nogami H., Schonbach C., Gojobori T.,
RA Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA Schirml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,
RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidae; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=12986/SvEvTac;
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Koltz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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CC -----
DR EMBL; AF371324; AAL50520.1; -; mRNA.
DR Ensembl; ENSMUSG00000063057; Mus musculus.
DR MGI; MGI:1928704; BaalC.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
SQ SEQUENCE 54 AA; 5667 MW; FE8C0E9FBCDB829 CRC64;

Query Match 38.3%; Score 294; DB 2; Length 54;
Best Local Similarity 100.0%; Pred. No. 7.2e-19;
Matches 54; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCGGSRADAIPRYESWTRETESTWLTYSDDALPSAAATDSGPAGGLHAG 54
DB 1 MCGGSRADAIPRYESWTRETESTWLTYSDDALPSAAATDSGPAGGLHAG 54

RESULT 10
QBWXSO HUMAN
ID QBWXSO HUMAN PRELIMINARY; PRT; 73 AA.
AC QBWXSO;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE BAALC 1-4-5-6-8.
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Koltz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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CC -----
DR EMBL; AF371324; AAL50380.1; -; Genomic DNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
SQ SEQUENCE 73 AA; 7871 MW; 98DBC2B6E5BF524A CRC64;

Query Match 37.5%; Score 288; DB 2; Length 73;
Best Local Similarity 91.4%; Pred. No. 3.5e-18;
Matches 53; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 MCGGSRADAIPRYESWTRETESTWLTYSDDALPSAAATDSGPAGGLHAG 58

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DB 1 MCGGSRADAIPRYESWTRETESTWLTYSDDALPSAAATDSGPAGGLHAG 58

RESULT 11
QBWTP6 HUMAN
ID QBWTP6 HUMAN PRELIMINARY; PRT; 54 AA.
AC QBWTP6;
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 13.
DE BAALC isoform 1-8 (Brain and acute leukemia, cytoplasmic, isoform 2)
DE (BAALC 1-8).
GN Name=BAALC;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Koltz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
RT "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906(2001).
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CC -----
DR EMBL; AF371323; AAL50519.1; -; mRNA.
DR EMBL; BC035038; AAL5038.1; -; Genomic DNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR GO; GO:0005737; C:cytoplasm; IDA.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
SQ SEQUENCE 54 AA; 5663 MW; FEF0B4EABED9B829 CRC64;

Query Match 36.2%; Score 278; DB 2; Length 54;
Best Local Similarity 94.4%; Pred. No. 2e-17;
Matches 51; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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DR EMBL; AF371326; AAL50522.1; -, mRNA.
DR InterPro; IPR009728; BAALC N; 1.
DR Pfam; PF06989; BAALC N; 1.
SQ SEQUENCE 54 AA; 5681 MW; 6538C3DABED9B825 CRC64;

Query Match 34.8%; Score 267; DB 2; Length 54;
Best Local Similarity 92.6%; Pred. No. 1.9e-16;
Matches 50; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIEPRYYESWTRETESTWLTYTSDALPSAAATDSGPEAGGLHAG 54
Db 1 MCGGSRADAIEPRYYESWTRETESTWLTYTSDALPSAAATDSGPEAGGLHAG 54

RESULT 12
Q8WXS2 HUMAN
ID Q8WXS2_HUMAN PRELIMINARY; PRT; 80 AA.
AC Q8WXS2
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE BAALC 1-2.
GN Name=BAALC;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
RA "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
CC -----
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CC -----
DR EMBL; AF363578; AAL50382.1; -, Genomic DNA.
DR Ensembl; ENSG00000164929; Homo sapiens.
DR InterPro; IPR009728; BAALC N.
DR Pfam; PF06989; BAALC N; 1.
SQ SEQUENCE 80 AA; 8573 MW; 70B89B91C3245E2D CRC64;

Query Match 35.5%; Score 272; DB 2; Length 80;
Best Local Similarity 94.3%; Pred. No. 1.1e-16;
Matches 50; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIEPRYYESWTRETESTWLTYTSDALPSAAATDSGPEAGGLHAG 53
Db 1 MCGGSRADAIEPRYYESWTRETESTWLTYTSDALPSAAATDSGPEAGGLHAG 53

RESULT 13
Q8WNE8_PIG
ID Q8WNE8_PIG PRELIMINARY; PRT; 54 AA.
AC Q8WNE8
DT 01-MAR-2002, integrated into UniProtKB/TrEMBL.
DT 01-MAR-2002, sequence version 1.
DT 07-FEB-2006, entry version 10.
DE BAALC isoform 1-8.
GN Name=BAALC;
OS Sus scrofa (Pig);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21574584; PubMed=11707601; DOI=10.1073/pnas.241525498;
RA Tanner S.M., Austin J.L., Leone G., Rush L.J., Plass C., Heinonen K.,
RA Mrozek K., Sill H., Knuutila S., Kolitz J.E., Archer K.J.,
RA Caligiuri M.A., Bloomfield C.D., de la Chapelle A.;
RA "BAALC, the human member of a novel mammalian neuroectoderm gene
RT lineage, is implicated in hematopoiesis and acute leukemia.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:13901-13906 (2001).
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CC -----
DR EMBL; AF371326; AAL50522.1; -, mRNA.
DR InterPro; IPR009728; BAALC N; 1.
DR Pfam; PF06989; BAALC N; 1.
SQ SEQUENCE 54 AA; 5681 MW; 6538C3DABED9B825 CRC64;

Query Match 34.8%; Score 267; DB 2; Length 54;
Best Local Similarity 92.6%; Pred. No. 1.9e-16;
Matches 50; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MCGGSRADAIEPRYYESWTRETESTWLTYTSDALPSAAATDSGPEAGGLHAG 54
Db 1 MCGGSRADAIEPRYYESWTRETESTWLTYTSDALPSAAATDSGPEAGGLHAG 54

RESULT 14
Q4RR60_TETNG
ID Q4RR60_TETNG PRELIMINARY; PRT; 51 AA.
AC Q4RR60
DT 19-JUL-2005, integrated into UniProtKB/TrEMBL.
DT 19-JUL-2005, sequence version 1.
DT 07-FEB-2006, entry version 4.
DE Chromosome 14 SCAF15003, whole genome shotgun sequence. (Fragment).
GN ORFNames=GSTENG00030307001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15496914; DOI=10.1038/nature03025;
RA Jaillon O., Aury J.-M., Brunet F., Petit J.-L., Stange-Thomann N.,
RA Micaudi E., Bouneau L., Fischer C., Ozoug-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Blomont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Brottier P., Coutanceau J.-P., Gouzy J.,
RA Parra G., Lardet V., Chappie C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Volff J.-N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissbach J., Roest Crollius H.;
RT "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
the early vertebrate proto-karyotype.";
RL Nature 431:946-957 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
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CC -----
DR EMBL; CAAB01015003; CAG09122.1; -, Genomic DNA.
FT NON TER 1 1
FT NON TER 51 51
SQ SEQUENCE 51 AA; 5504 MW; F220296F4E99153C CRC64;

Query Match 21.7%; Score 166.5; DB 2; Length 51;
Best Local Similarity 65.3%; Pred. No. 1.8e-07;
Matches 32; Conservative 6; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MCGGSRADAIEPRYYESWTRETESTWLTYTSDALPSAAATDSGPEAG 49
Db 3 MCGGSRDALAPLYESWTRETESTWLTYTSDALPSAAATDSGPEAG 50
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RESULT 15
QB01V5_BRARE PRELIMINARY; PRT; 32 AA.
ID QB01V5;
AC QB01V5;
DT 01-JUN-2003, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2003, sequence version 1.
DT 07-FEB-2006, entry version 9.
DE Novel protein similar to human brain and acute leukemia, cytoplasmic
DE (BAALC) (Fragment).
GN Name=baalc; Synonyms=OTTDPAR0000001859; ORFNames=zC215113.3-001;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Sehra H.;
RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AL807244; CAD87801.1; -; Genomic_DNA.
DR ZFIN; ZDB-GENE-030616-613; baalc.
DR InterPro; IPR009728; BAALC_N.
DR Pfam; PF06989; BAALC_N; 1.
FT NON_TER 32
FT 32
SQ SEQUENCE 32 AA; 3663 MW; 916A5445D263B7P7 CRC64;

Query Match 21.0%; Score 161; DB 2; Length 32;
Best Local Similarity 90.6%; Pred. No. 3.3e-07;
Matches 29; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MCGGSRADAIEPRYVESWTRETESTLTNTD 32
DB 1 MCGGSRADAIEPRYQESWTRETESTLTNTTE 32

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Search completed: May 20, 2006, 20:26:16
Job time : 301 secs

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